

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat May 13 09:58:28 2000; Maspar time 4.62 Seconds
230.882 Million cell updates/sec
Tabular output not generated.

Title: >US-09-331-631-3
Description: (29-73) from US09331631.pep (2 of 5)
Perfect Score: 361
Sequence: 1 SEFDRQYECKRCQCMQLETSQMRVCVSCQDKRFEEDIDMSKYD 45

Scoring table:
Gap 11
PAM 150

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:geneseqp

Statistics: Mean 24.753; Variance 88.190; scale 0.281

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	361	100.0	666	1	Macadamia integrifolia	2.58e-30
2	361	100.0	666	1	Macadamia integrifolia	2.58e-30
3	259	71.7	625	1	Macadamia integrifolia	9.96e-19
4	109	30.2	590	1	Gossypium hirsutum ant	1.26e-02
5	97	26.9	525	1	Theobroma cacao antim	1.88e-01
6	97	26.9	566	1	Sequence encoded by 67	1.88e-01
7	95	26.3	218	1	Human TSP1 protein	2.93e-01
8	95	26.3	239	1	Human thrombospondin 1	2.93e-01
9	95	26.3	441	1	Human concanavalin T	2.93e-01
10	77	21.3	62	1	Maize id gene product	1.39e+01
11	77	21.3	409	1	G. max truncated SBP2	1.39e+01
12	77	21.3	438	1	Maize id protein	1.39e+01
13	77	21.3	444	1	G. max truncated SBP1	1.39e+01
14	77	21.3	489	1	G. max SBP2 protein	1.39e+01
15	77	21.3	524	1	G. max SBP1 protein	1.39e+01
16	73	20.2	81	1	Human 5' EST secreted	3.18e+01
17	73	20.2	125	1	HE4 epididymis-specific	3.18e+01
18	73	20.2	125	1	Human HE4 protein	3.18e+01
19	73	20.2	1284	1	Sequence encoded by a	3.90e+01
20	72	19.9	593	1	zebra mays antimicrobial	3.90e+01
21	72	19.9	1416	1	Human astrovirus serot	3.90e+01
22	71	19.7	2703	1	P. falciparum Proj3.	4.77e+01
23	71	19.7	2710	1	Plasmodium Proj3.	4.77e+01

ID	Score	Query Match	Length	ID	Description	Pred. No.
24	71	19.7	3060	1	Plasmodium var-7.	4.77e+01
25	70	19.4	103	1	Human 5' EST secreted	5.83e+01
26	70	19.4	348	1	N. gonorrhoeae glycosyl	5.83e+01
27	70	19.4	348	1	Neisseria polyglycosyl	5.83e+01
28	69	19.1	33	1	zebra mays antimicrobial	7.13e+01
29	69	19.1	35	1	Antimicrobial maize pe	7.13e+01
30	68	18.8	623	1	Arabidopsis enhanced d	8.70e+01
31	68	18.8	816	1	WD-40 domain-contg. Mu	8.70e+01
32	68	18.8	1479	1	Human type C lectin	8.70e+01
33	67	18.6	203	1	Mycobacterium species	1.06e+02
34	67	18.6	363	1	ITV thymidine kinase	1.06e+02
35	67	18.6	506	1	Mycobacterium species	1.06e+02
36	67	18.6	974	1	Human transient recept	1.06e+02
37	66	18.3	30	1	(Cyclo 30-33)ID-Phe12,	1.29e+02
38	66	18.3	38	1	Cyclic corticotrophin	1.29e+02
39	66	18.3	194	1	P. aeruginosa muca.	1.29e+02
40	66	18.3	370	1	Homo sapiens B23 sequ	1.29e+02
41	66	18.3	676	1	Thermus aquaticus DNA	1.29e+02
42	66	18.3	676	1	A thermophilic ligase	1.29e+02
43	66	18.3	680	1	Thermostable T. aquat	1.29e+02
44	66	18.3	1496	1	Human silt 3 mature pr	1.29e+02
45	66	18.3	1523	1	Human silt 3 protein.	1.29e+02

ALIGNMENTS

RESULT 1
ID W62829 standard; Protein: 666 AA.
AC W62829;
DI 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH key
FT Peptide
FT Protein
FT Protein
FT Protein
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (REPR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Mannens JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 39-41; 96PP; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;
Query Match 100.0%; Score 361; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.58e-30;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 SEFDRQYECKRCQCMQLETSQMRVCVSCQDKRFEEDIDMSKYD 73
QY 29 SEFDRQYECKRCQCMQLETSQMRVCVSCQDKRFEEDIDMSKYD 73

RESULT 2
ID W62828 standard; Protein: 666 AA.
AC W62828;
DI 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH key
FT Peptide
FT Protein
FT Protein
FT Protein
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (REPR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Mannens JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 39-41; 96PP; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;
Query Match 100.0%; Score 361; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.58e-30;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FT Protein 29.666
FT /note="mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42310.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 34-36; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 100.0%; Score 361; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.58e-30;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 29 SFEDROEYECRCQCMOLETSGOMRCVSCDCKREEDIDMSKYD 73
OY 29 SEFDROEYECRCQCMOLETSGOMRCVSCDCKREEDIDMSKYD 73

RESULT 3
ID W62830 standard; Protein; 625 AA.
AC W62830.
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note="signal peptide"
FT Protein 29..666
FT /note="mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42316.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 43-45; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 625 AA;

Query Match 71.7%; Score 259; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 9.96e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 OCMOLETSGOMRCVSCDCKREEDIDMSKYD 32
OY 42 OCMOLETSGOMRCVSCDCKREEDIDMSKYD 73

RESULT 4
ID W62832 standard; Protein; 590 AA.
AC W62832.
DT 27-OCT-1998 (first entry)
DE Gossypium hirsutum antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Gossypium hirsutum.
PN W09827805-A1.
PD 02-JUL-1998.

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PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 49-51; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 590 AA;

Query Match 30.2%; Score 109; DB 1; Length 590;
Best Local Similarity 45.2%; Pred. No. 1.26e-02;
Matches 14; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

DB 87 YEECQECRCQDEER-QQPCQCRCLKREOE 116
OY 36 YEECQRCQCMOLETSGOMRCVSCDCKREED 66

RESULT 5
ID W62831 standard; Protein; 525 AA.
AC W62831.
DT 27-OCT-1998 (first entry)
DE Theobroma cacao antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Theobroma cacao.
PN W09827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 47-49; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 525 AA;

Query Match 26.9%; Score 97; DB 1; Length 525;
Best Local Similarity 31.4%; Pred. No. 1.88e-01;
Matches 11; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

DB 39 ROVEYQCRCRCESEXTEREQCEQRCEREYKQ 73
OY 33 ROVEYECRCQCMOLETSGOMR-RCVSQCDCKREED 66

RESULT 6
ID R20181 standard; Protein; 566 AA.
AC R20181.
DT 16-APR-1992 (first entry)
DE Sequence encoded by 67 kD T. cacao protein cDNA.
KW Cocoa; flavour; vicillin; seed storage protein.
OS Theobroma cacao.
PN W09119801-A.
PD 26-DEC-1991.
PE 07-JUN-1991; G00914.
PR 11-JUN-1990; GB-013016.
PA (MRSC) MARS UK LTD.
PI Spencer ME, Hodge R, Deakin EA, Ashton S;
DR WPI: 92-024418/03.
PT Recombinant cocoa proteins - are responsible for flavour in cocoa
PT beans and produced in large quantities using yeast and bacterial
PT expression vectors.
PS Claim 4; Fig 2; 59pp; English.
CC The inventors claim a 67 kD and 31 kD T. cacao protein, and

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Db 116 SSVQTRTCHIQECDKRFKODGWS 139
 :| | | :| | | | | :| |
 OY 48 TSGOMRRC-VSQCDKRFEDIDW 70

RESULT 10
 ID W03698 standard; Protein: 62 AA.

AC W03698;
 DT 06-MAR-1997 (first entry)
 DE Maize id gene product.
 KW Maize; Zea mays; Id; id*; transposon; transposable element;
 KM Ds2; flower evocation; zinc-finger regulatory protein.
 OS Zea mays.

PN W09634088-A2.
 PD 31-OCT-1996.
 PF 15-MAR-1996; U03466.
 PR 16-MAR-1995; US-406186.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Colasanti JJ, Sundaresan V;
 DR WPI: 96-497621/49.

DR N-PSDB; T42174, T42175.

PT New isolated plant id gene - used to develop prods. for use in altering the induction of flowering in plants

PS Claim 7; Fig 3 and Fig 5; 58pp: English.
 CC The id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zinc-finger regulatory proteins in animals.

CC Transposons Ac and Ds constitute a family of related transposable elements present in maize. A derivative of Ds, Ds2, can be used to produce a new mutant of the id gene. The Ds2 (in the presence of active Ac) is excised from a nearby gene on chromosome 1 and inserted into the id gene to produce id*.
 CC Sequence 62 AA;

Query Match 21.3%; Score 77; DB 1; Length 62;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 17 GKRWCRCRGKPYAVOSDW 36
 :| | | :| | | :| |
 OY 50 GOMRRCVSCDKRFEDIDW 69

RESULT 11
 ID W90342 standard; Protein: 409 AA.

AC W90342;
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP2 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 OS Glycine max.

PN W09853086-A1.
 PD 26-NOV-1998.
 PF 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI: 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds

PS Claim 7; Page 39-40; 58pp: English.
 CC This sequence represents a novel sucrose binding protein, SBP2, isolated from glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP.

CC The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content

CC of the seed (e.g. where the seed is the primary plant material harvested, CC such as soybean). In contrast, decreased sucrose uptake activity in CC seeds might be desirable where the vegetative material of the plant is CC harvested. The SBP regulatory regions confer specific or enhanced CC expression in developing seeds and so may be used to express any CC transgene in developing seeds.
 SO Sequence 409 AA;

Query Match 21.3%; Score 77; DB 1; Length 409;
 Best Local Similarity 45.8%; Pred. No. 1.39e+01;
 Matches 11; Conservative 6; Mismatches 5; Indels 2; Gaps 2;

Db 42 CKHCCGQGRQYTESDKRTLOQCD 65
 :| | | | :| | | | | :| |
 OY 39 CKRCQMQL-E-TSGMRRCVSCD 60

RESULT 12
 ID W59836 standard; Protein: 438 AA.

AC W59836;
 DT 16-NOV-1998 (first entry)
 DE Maize id protein.
 KW Maize; Id; floral induction; transgenic plant.
 OS Zea mays.

PN W09837201-A1.
 PD 27-AUG-1998.
 PF 18-FEB-1998; U03161.
 PR 30-DEC-1997; US-000640.
 PR 20-FEB-1997; US-804104.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Colasanti JJ, Sundaresan V;
 DR WPI: 96-467364/40.

DR N-PSDB; V41721.
 PT Id gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops

PS Claim 5; Fig 3; 68pp: English.
 CC The maize id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The id gene and zinc-finger regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in id detection e.g. to locate activity in plants.

CC Sequence 438 AA;
 Query Match 21.3%; Score 77; DB 1; Length 438;
 Best Local Similarity 35.0%; Pred. No. 1.39e+01;
 Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 187 GKRWCRCRGKPYAVOSDW 206
 :| | | | :| | | :| |
 OY 50 GOMRRCVSCDKRFEDIDW 69

RESULT 13
 ID W90340 standard; Protein: 444 AA.

AC W90340;
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP1 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 OS Glycine max.

PN W09853086-A1.
 PD 26-NOV-1998.
 PF 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI: 99-070155/06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds

PS Claim 7: Page 36-37, 58bp; English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
CC Sequence 444 AA:

Query Match	21.38;	Score 77;	DB 1;	Length 444;
Best Local Similarity	44.48;	Pred. No. 1.39e+01;		
Matches	12;	Conservative	6;	Mismatches 6;
				Indels 3;
				Gaps 2;

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Db      43  CKHCCQQQQQYTEGDKRVCLQSCD-RY 68
      ||:| |:| |:| |:| |:|
QY     39  CKRQCMQLE-TSGQMRRCVSVQCDKRF 63
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RESULT 14
ID M90341 standard; protein: 489 AA.
AC M90341;
DT 24-MAY-1999 (first entry)
DE G.-max SBP2 protein.
KW SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;
KM seed: carbohydrate content; soybean.
OS Glycine max.
SN M09853086-A1.
PN 26-NOV-1998.
PD 21-MAY-1998; 010465.
PE 22-MAY-1997; US-047568.
PR (UNIM) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI: 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 13b: Page 37-38; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
CC Sequence 489 AA:
CC

Query Match 21.3%; Score 77; DB 1; Length 489;
Best Local Similarity 45.8%; Pred. No. 1.39e+01;
Matches 11; Conservative 6; Mismatches 5; Indels 2; Gaps 2;

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Db      42 CKHCCQQQRQYTESDKRTCLQQCD 65
      11::11 | : | ::1 | : 111
QY     39 CKRQCMQL-E-TSGQMRRCVSSQCD 60
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RESULT 15
 ID W90339 standard: protein: 524 AA.
 AC W90339;
 DT 24-MAY-1999 (first entry)
 DE G. max SBP1 protein.
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KW seed; carbohydrate content; soybean.
 OS Glycine max.
 PN W08853086-A1.
 PN 26-NOV-1998.
 PF 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD.
 DR WPI: 99-070155/06.
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 PS Disclosure: Page 34-36: 58pp: English.
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated
 CC from Glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC Sequence 524 AA:

Query Match	21.3%;	Score 77;	DB 1;	Length 524;
Best Local Similarity	44.4%;	Pred. No. 1.39e+01;		
Matches	12;	Conservative	6;	Mismatches 6;
			Indels 3;	Gaps 2;

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Db      43 CKHCCQQQQQYTEGDKRVCLQSCD-RY 68
      11:111:111:111:
QY     39 CKRQCMQLE-TSGQMRRCVSOCDKRF 63

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Search completed: Sat May 13 09:58:37 2000
Job time : 9 secs.

